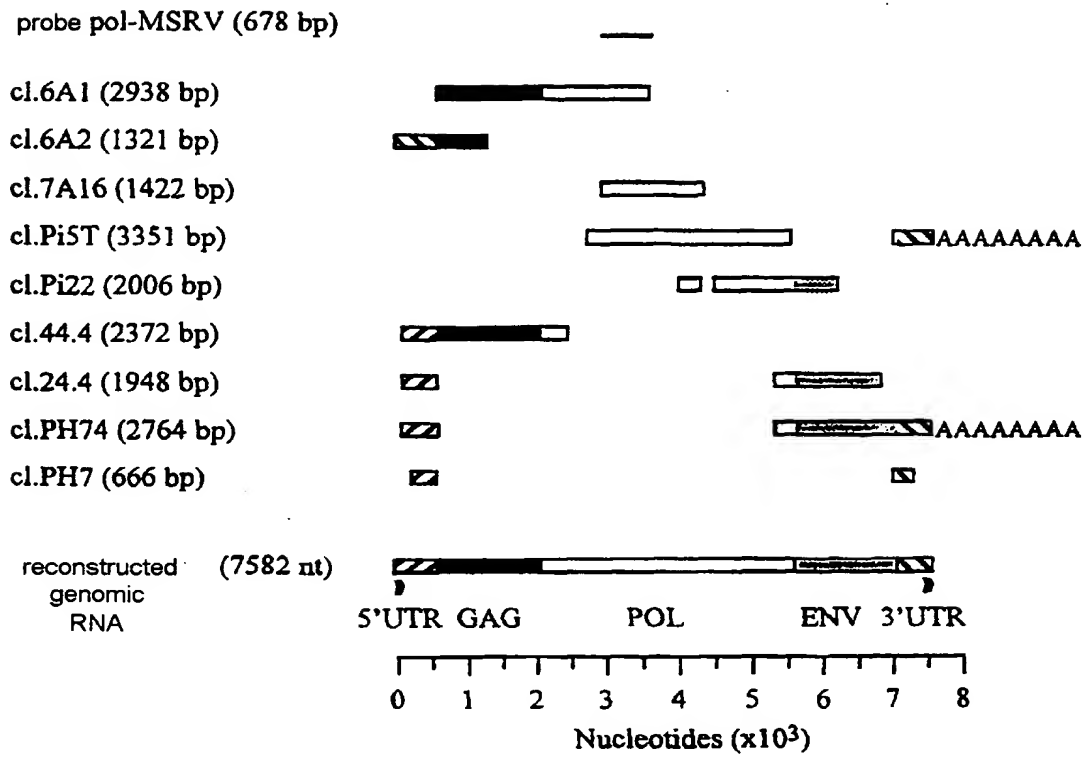


FIG 1



09/446024-12094460

[illegible]

Probes

PS'env-cl.24.4 Ppagg-LB19 Pro-E Pool-MSRV Penv-CI5

P5' gag-cl.6A2

FIG 3


					
1	_____	7582	Names Recons RNA	Similarities	Repetitions
28274	_____	37879	RG083M05 [7]	96%	yes
6911	_____	14079	BAC378 [14]	88%	yes
35199	_____	27999	Q11M15 [21]	89%	yes
91239	_____	94627	U134E6 [x]	88%	no
					ORFs
					538
					538
					no
					413 and 305
					no

FIG 4A

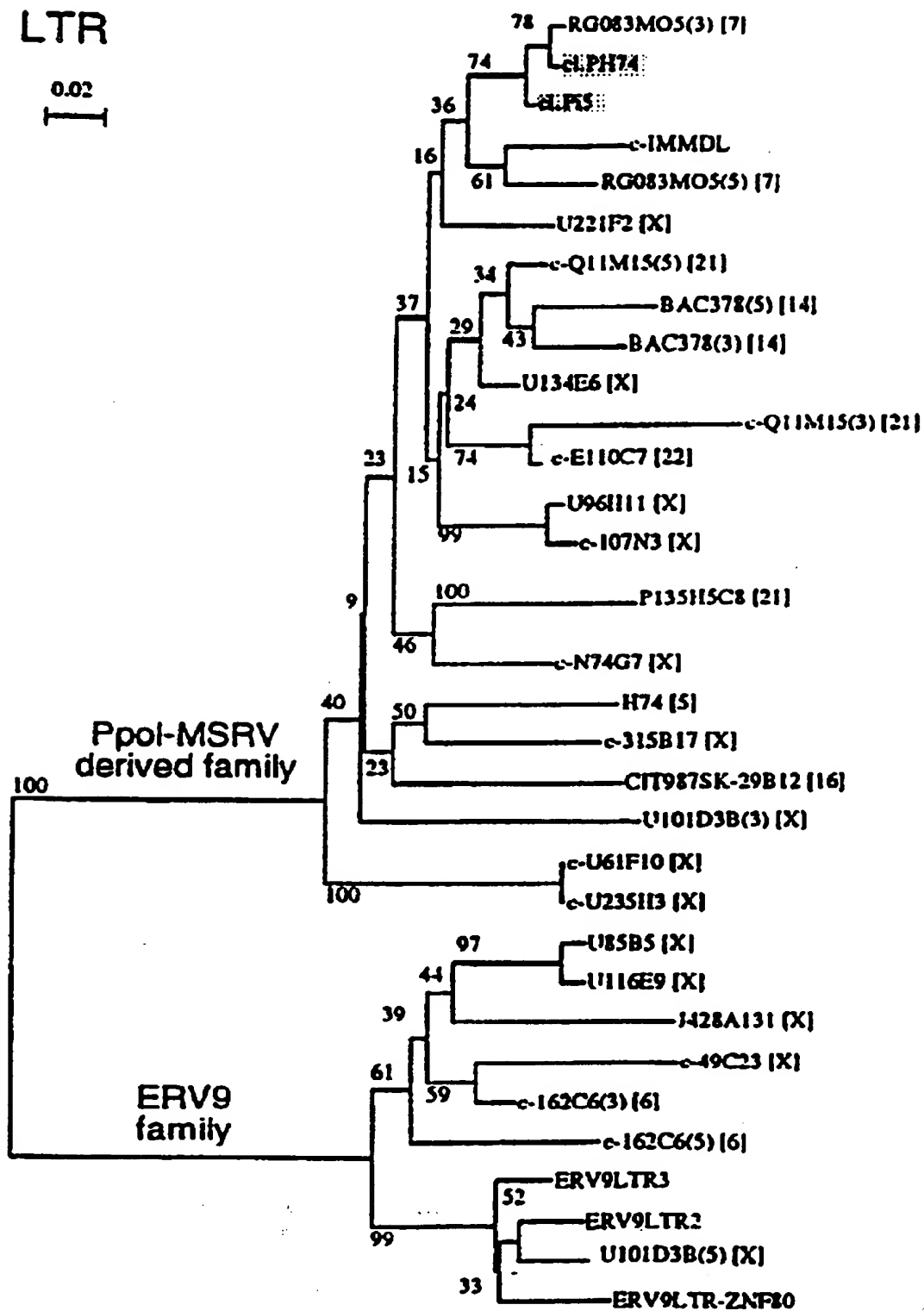
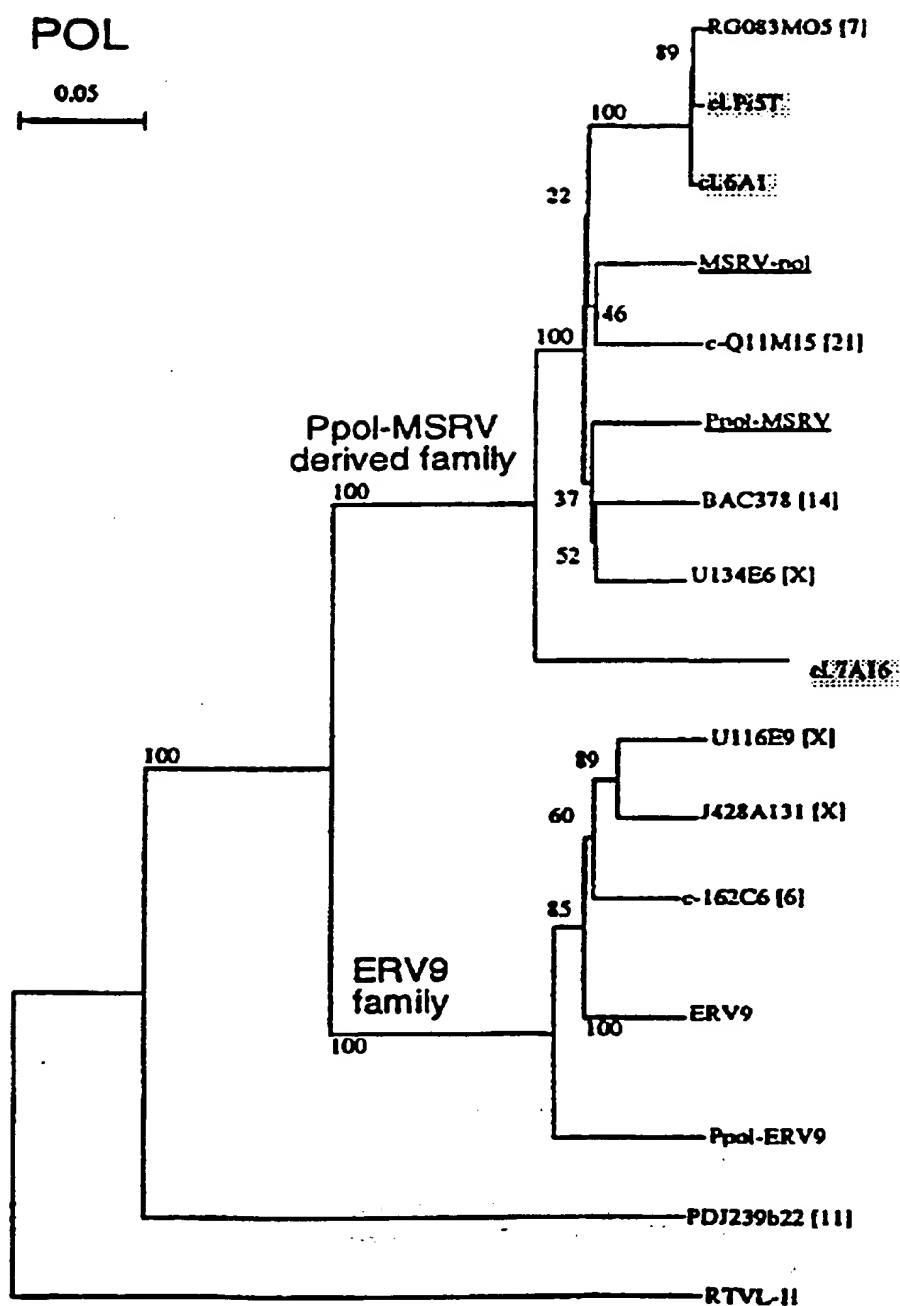
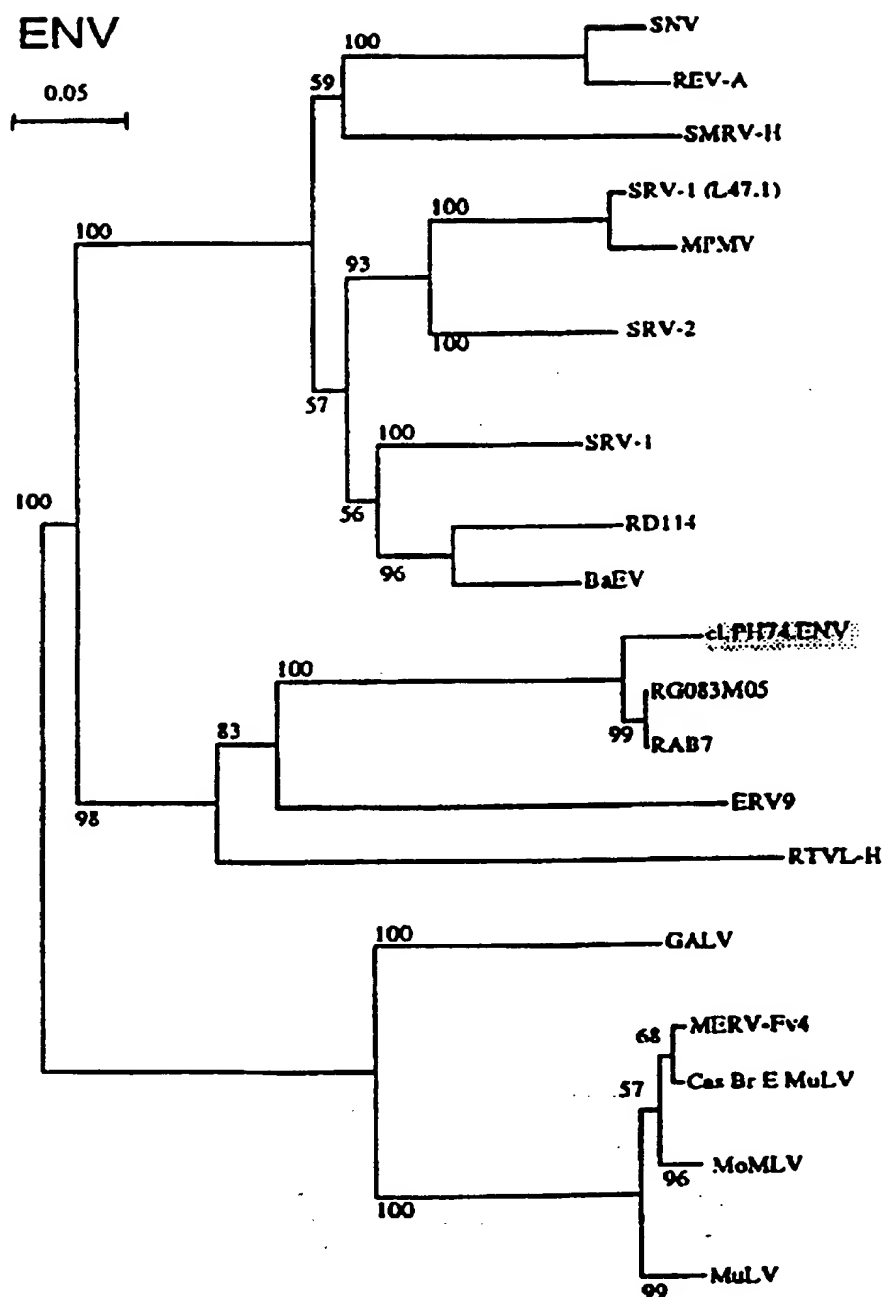


FIG 4 B



ENV



06-09-70

FIG 5A

5-RG-28000-28872
3-RG-37500-38314
3-PH74.2359-2782
3-C4C5.710-1136
Consensus
5-RG-28000-28872
3-RG-37500-38314
3-PH74.2359-2782
3-C4C5.710-1136
Consensus
5-RG-28000-28872
3-RG-37500-38314
3-PH74.2359-2782
3-C4C5.710-1136
5-6A2.1-600
5-PH74.1-530
Consensus
5-RG-28000-28872
3-RG-37500-38314
3-PH74.2359-2782
3-C4C5.710-1136
5-6A2.1-600
5-PH74.1-530
4.1-486
Consensus
5-RG-28000-28872
3-RG-37500-38314
3-PH74.2359-2782
3-C4C5.710-1136
5-6A2.1-600
5-PH74.1-530
5-24.4.1-486
Consensus

585	5'-RG-28000-28872	CCGCAGACCTGGCCGCTGACCTCCCAATCCCTCTGGAATCTCCAGGGGTGTCCTGATGCTCCAGCGAGGCGGCCCAATTGCGCGCTCCCAATTGCGGCTTAAAGGCTTGGCCCAATTGTTCTCTGC	760	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC
572	3'-RG-37500-38314	CCGACAGACCCGCGCTGACCTCCCAATCCCTCTGGAATCTCCAGGGGTGTCCTGATGCTCCAGCGAGGCGGCCCAATTGCGCGCTCCCAATTGCGGCTTAAAGGCTTGGCCCAATTGTTCTCTGC	766	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC
312	5'-6A2.1-600	CCGACAGACCTGGCCGCTGACCTCCCAATCCCTCTGGAATCTCCAGGGGTGTCCTGATGCTCCAGCGAGGCGGCCCAATTGCGCGCTCCCAATTGCGGCTTAAAGGCTTGGCCCAATTGTTCTCTGC	551	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC
241	5'-PH74.1-530	CCGACAGACCTGGCCGCTGACCTCCCAATCCCTCTGGAATCTCCAGGGGTGTCCTGATGCTCCAGCGAGGCGGCCCAATTGCGCGCTCCCAATTGCGGCTTAAAGGCTTGGCCCAATTGTTCTCTGC	481	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC
198	5'-5-24.4.1-486	CCGACAGACCTGGCCGCTGACCTCCCAATCCCTCTGGAATCTCCAGGGGTGTCCTGATGCTCCAGCGAGGCGGCCCAATTGCGCGCTCCCAATTGCGGCTTAAAGGCTTGGCCCAATTGTTCTCTGC	437	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC
520	Consensus	CCGACAGACCTGGCCGCTGACCTCCCAATCCCTCTGGAATCTCCAGGGGTGTCCTGATGCTCCAGCGAGGCGGCCCAATTGCGCGCTCCCAATTGCGGCTTAAAGGCTTGGCCCAATTGTTCTCTGC		Consensus
705	5'-RG-28000-28872	ACGGCTAAGTGCCCTGGGTTTGTCTTAATTGAGCTGAACTAGTCACTGCGGTTCCATGCGTTCTCTCTGTGTACCCAGCGCTTCTTAATGAGACTATTAACACTTAAACACATGAGGCCCAAGATT		
692	3'-RG-37500-38314	ATGCGCTAAGTGCCCTGGGTTTGTCTTAATTGAGCTGAACTAGTCACTGCGGTTCCATGCGTTCTCTCTGTGTACCCAGCGCTTCTTAATGAGACTATTAACACTTAAACACATGAGGCCCAAGATT		
432	5'-6A2.1-600	ACGGCTAAGTGCCCTGGGTTTGTCTTAATTGAGCTGAACTAGTCACTGCGGTTCCATGCGTTCTCTCTGTGTACCCAGCGCTTCTTAATGAGACTATTAACACTTAAACACATGAGGCCCAAGATT		
361	5'-PH74.1-530	ACGGCTAAGTGCCCTGGGTTTGTCTTAATTGAGCTGAACTAGTCACTGCGGTTCCATGCGTTCTCTCTGTGTACCCAGCGCTTCTTAATGAGACTATTAACACTTAAACACATGAGGCCCAAGATT		
318	5'-5-24.4.1-486	ACGGCTAAGTGCCCTGGGTTTGTCTTAATTGAGCTGAACTAGTCACTGCGGTTCCATGCGTTCTCTCTGTGTACCCAGCGCTTCTTAATGAGACTATTAACACTTAAACACATGAGGCCCAAGATT		
640	Consensus	ATGCGCTAAGTGCCCTGGGTTTGTCTTAATTGAGCTGAACTAGTCACTGCGGTTCCATGCGTTCTCTCTGTGTACCCAGCGCTTCTTAATGAGACTATTAACACTTAAACACATGAGGCCCAAGATT		
824	5'-RG-28000-28872	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC		
766	3'-RG-37500-38314	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC		
551	5'-6A2.1-600	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC		
481	5'-PH74.1-530	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC		
437	5'-24.4.1-486	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC		
760	Consensus	CCATTCTTGGAAATCTCTTRANGSOMAGCAATTCALSTCTGAGGAAATACGARGCTTGGCCACCAATCTTGGAAAGCGGCGCTCTCTACCAATCTTGGAAAGCTTTCACCAACCAATCTTGGGAGGCTCTGC		
	5'-RG-28000-28872	TTGACGAAGGACCCCGGTAACATTTTGGCAACCAAGGAGGACATCCA	873	
	3'-RG-37500-38314	TTGACGAAGGACCCCGGTAACATTTTGGCAACCAAGGAGGACATCCA	815	
	5'-6A2.1-600	TTGACGAAGGACCCCGGTAACATTTTGGCAACCAAGGAGGACATCCA	600	
	5'-PH74.1-530	TTGACGAAGGACCCCGGTAACATTTTGGCAACCAAGGAGGACATCCA	530	
	5'-24.4.1-486	TTGACGAAGGACCCCGGTAACATTTTGGCAACCAAGGAGGACATCCA	486	
	Consensus	TTGACGAAGGACCCCGGTAACATTTTGGCAACCAAGGAGGACATCCA	783	

Conclusions

ORF1: ENV (538 AA) FIG 6

```

<--- L ---><--- SU
MGLPYHIFLCVLSPCFTLTAPPPCRCMTSSSPHPEFLWRMQRPGNIDAPSYRSLSKGTP 60
A FT V S YQ C

TFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCPGGLGVTVCWTFYFTQTGMSDGGGV 120

QDQAREKHVKEVISQLTGVTGTSPPYKGLDLSKLHETLRTHTRLVSLFNTTLTGLHEVSA 180
R

QNPTNCWICLPLNFRPYVSIPVPEQWNNPSTEINTTSVLVGPLVSNVEITHTSNLTVCVKF 240
L

SNTTYTTNSQCIRWVTPPTQIVCLPSGIFFVCGTSAYRCLNGSSESMCFLSFLVPPMAIY 300
T

TEQDLYSYVISKPRNKRVPILPFVIGAGVLGALGTGIGGITTSTQFYKLSQELNGDMER 360
TM

VADSLVTLQDQLNSLA AVLQNRALDLLTAERGGTCLFLGEECCYYVNQSGIVTEKVEE 420
R S K

IPDRIQRIAEELRNTGPWGLLSRWMPWILPFLGPLAAIILLLLFGPCIFDLLVNFVSSRI 480
R R Q N

EAVKLQMEPKMQSKTKIYRRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS 538
-->

```

ORF2 (52AA)

MEPKMQSKTKIYRRPLDRPVSPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS-

Alignment ORF2 and Rex PLLV-L

```

ORF2          KIY-RRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRP
++Y   LD P SP ++           P S QPLLRP
Rex PTLV-L (B53482) RLYNTLSLDSPPSPPKELPA-----PSRFSPPQPLLRP

```

ORF3 (48AA)

MLMTSKAPLLRKSQHLNLYYAPIQQEAVRAVVGQPPQQLGFPVEMGD

Alignment ORF3 and Tat SIV-AGM

```

ORF3          MTSKAPLLRKSQHLNLYYAPIQQEAVRAVVGQPPQ
+T AP R+ ++ +L AP+Q +++ G+ Q
Tat SIV-AGM(p05913) VTYHAPRTRRKKIRSLNLAPLQHSISTKWGRDQ

```

00446024 "42094460